

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2540	100.0	468	5	Q9BMH3	ichthyophth
2	921	36.3	442	5	Q9XZG2	ichthyophth
3	878	34.6	460	5	Q962N5	ichthyophth
4	775.5	30.5	395	5	Q27208	ichthyophth
5	345	13.6	371	5	Q9GPP0	tetrahymena
6	289.5	11.4	316	5	Q9GPP3	tetrahymena
7	286.5	11.3	316	5	Q9GPP4	tetrahymena
8	283.5	11.2	305	5	Q9GPP2	tetrahymena
9	236	9.3	594	5	Q24970	giardia lam
10	232	9.1	645	5	Q97448	giardia lam
11	228	9.0	1274	5	Q24977	giardia lam
12	227.5	9.0	667	5	Q9XTK3	giardia lam
13	226	8.9	719	5	Q90019	giardia lam
14	221.5	8.7	719	5	Q90021	giardia lam
15	219	8.6	1274	5	Q9NGL3	giardia lam
16	218.5	8.6	548	5	Q9GQ45	giardia lam

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QY 181 RSFTECVKRLNLYNGNGTNPENPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVA 240
DB 181 RSFTECVKRLNLYNGNGTNPENPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVA 240
QY 241 CPDGTISAAGVNNWVAQNTCTNCAPNFYNNAPNPNPNSGNTCLPCPANKDYGAETAGG 300
DB 241 CPDGTISAAGVNNWVAQNTCTNCAPNFYNNAPNPNPNSGNTCLPCPANKDYGAETAGG 300
QY 301 AATLAKQCNIACPDGTATASGATNVILOTECLNCAANFYEDGNFQAGSSRCRCKACPANK 360
DB 301 AATLAKQCNIACPDGTATASGATNVILOTECLNCAANFYEDGNFQAGSSRCRCKACPANK 360
QY 361 VOGAVATAGGTATLIAQCALECPAGTTLTDTTSTYKQAASECVKCAANFYTTKTQDWVA 420
DB 361 VOGAVATAGGTATLIAQCALECPAGTTLTDTTSTYKQAASECVKCAANFYTTKTQDWVA 420
QY 421 GIDTCTSCNKKLTSGAANLPESAKKNIOCFDANFLSISLLISYLL 468
DB 421 GIDTCTSCNKKLTSGAANLPESAKKNIOCFDANFLSISLLISYLL 468

RESULT 2
Q9XZG2 PRELIMINARY; PRT; 442 AA.
AC Q9XZG2;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Immobilization antigen precursor.
GN IAG48.
OS Ichthyophthirius multifiliis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Ophryoglenina; Ichthyophthirius.
OX NCBI_TaxID=5932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G1;
RX MEDLINE=99196987; PubMed=10095108;
RA Clark T.G., Lin T.L., Jackwood D.A., Sherrill J., Lin Y.,
RA "Dickerson H.W.;
RA "The gene for an abundant parasite coat protein predicts tandemly
RT repetitive metal binding domains.";
RL Gene 229:91-100(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=G1;
RA Gaertig J., Gao Y., Tishgarten T., Clark T.G., Dickerson H.W.;
RT "Surface display of a parasite antigen in the ciliate Tetrahymena
RT thermophila.";
RL Nat. Biotechnol. 0:0-0(1999).
DR EMBL; AF140273; AAD31283.1; -.
DR PRINTS; PR01574; TUBBYPROTEIN.
KW Signal.
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 442 IMMOBILIZATION ANTIGEN.
SQ SEQUENCE 442 AA; 45025 MW; 52658F3F65D27AFA CRC64;

Query Match 36.3%; Score 921; DB 5; Length 442;
Best Local Similarity 41.8%; Pred. No. 2.3e-59;
Matches 214; Conservative 45; Mismatches 139; Indels 114; Gaps 19;

QY 1 MKNNILVILIISLFINQIKSANGCPVGTETNTAGQVD----DLGTPANCVCNKFNYYNA 56
DB 1 MKYNNILILIISLFINELRAVPCPDGTQTQ-AGLTDVGAADLGT--CVNCRPNFYNGG 56
QY 57 AAFVPGASTCTPCPKQKDGAGQPNPAPATANLVTCNVKCPAGTATAGGATYAAIITECV 116
DB 57 AA-----OGEANGNPPFAAN-----
QY 117 NCRINYNENAPNFNAGASTCTACPNRVYGGALTAGNAATIAQCNVACPTGALDDGVT 176
DB 72 -----NAARGICVPCQINRVGSVTNAGDLATATQCTQCTGTALDDGVT 117
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QY 177 TDYVRSETECVKRLNLYNGNGTNPENPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVA 221
DB 177 TDYVRSETECVKRLNLYNGNGTNPENPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVA 221
QY 222 VAOATLGNDAITIAQCNVACPDGTISAAAGVNNWVAQNTCTNCAPNFYNNAPNPNPNSGNTCLPCPANKDYGAETAGG 300
DB 222 VAOATLGNDAITIAQCNVACPDGTISAAAGVNNWVAQNTCTNCAPNFYNNAPNPNPNSGNTCLPCPANKDYGAETAGG 300
QY 301 AATLAKQCNIACPDGTATASGATNVILOTECLNCAANFYEDGNFQAGSSRCRCKACPANK 360
DB 301 AATLAKQCNIACPDGTATASGATNVILOTECLNCAANFYEDGNFQAGSSRCRCKACPANK 360
QY 361 VOGAVATAGGTATLIAQCALECPAGTTLTDTTSTYKQAASECVKCAANFYTTKTQDWVA 420
DB 361 VOGAVATAGGTATLIAQCALECPAGTTLTDTTSTYKQAASECVKCAANFYTTKTQDWVA 420
QY 421 GIDTCTSCNKKLTSGAANLPESAKKNIOCFDANFLSISLLISYLL 468
DB 421 GIDTCTSCNKKLTSGAANLPESAKKNIOCFDANFLSISLLISYLL 468

RESULT 3
Q962N5 PRELIMINARY; PRT; 460 AA.
AC Q962N5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 52kDa immobilization antigen variant B protein.
OS Ichthyophthirius multifiliis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Ophryoglenina; Ichthyophthirius.
OX NCBI_TaxID=5932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G5;
RA Lin Y., Wang J.C., Clark T.C.;
RT "Variation in primary sequence and tandem repeat copy number among i-
RT antigen genes of Ichthyophthirius multifiliis.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF405431; AAK94941.1; -.
SQ SEQUENCE 460 AA; 47535 MW; 55DB1FB3C62F2371 CRC64;

Query Match 34.6%; Score 878; DB 5; Length 460;
Best Local Similarity 37.3%; Pred. No. 3.2e-56;
Matches 192; Conservative 63; Mismatches 158; Indels 102; Gaps 15;

QY 1 MKNNILVILIISLFINQIKSANGCPVGTETNTAGQVD----DLGTPANCVCNKFNYYN-- 54
DB 1 MKFNILILIISLFINELRAVNCNGAAI-ANGOSDTGAADINT--CTHCQKHFFYNGG 56
QY 55 -----NAAAFVPGASTCTPCPKQKDGAGQPNPAPATANLVTCNVKCPAGTATAGGATD 107
DB 55 -----NAAAFVPGASTCTPCPKQKDGAGQPNPAPATANLVTCNVKCPAGTATAGGATD 107
QY 108 YAAIITECVNCRINFY-----NENAPNFNAGASTCT 138
DB 108 YAAIITECVNCRINFY-----NENAPNFNAGASTCT 138
QY 139 ACYPNVGGALTAGNAATIAQCNVACPTGALDDGVTDDYVRSFTECVKRLNLYNGNGTNPENPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVA 240
DB 139 ACYPNVGGALTAGNAATIAQCNVACPTGALDDGVTDDYVRSFTECVKRLNLYNGNGTNPENPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVA 240
QY 176 ACQVKNKSDSQLRPGQAQANLATQCNNECPTGTATQDGAIFITYQSISQCTCKVDYFNGG 235
DB 176 ACQVKNKSDSQLRPGQAQANLATQCNNECPTGTATQDGAIFITYQSISQCTCKVDYFNGG 235
QY 199 NGNTPFNPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVACPDGTISAAAGVNNWVAQNTCTNCAPNFYNNAPNPNPNSGNTCLPCPANKDYGAETAGG 300
DB 199 NGNTPFNPGKSQCTPCPAKPANVAQATLGNDAITIAQCNVACPDGTISAAAGVNNWVAQNTCTNCAPNFYNNAPNPNPNSGNTCLPCPANKDYGAETAGG 300
QY 236 NPSAQ-NPFGNGQFTP-----GQLIANPDATAAQIPW----- 267
DB 236 NPSAQ-NPFGNGQFTP-----GQLIANPDATAAQIPW----- 267
QY 259 TECTNCAPNFYNNAPNFNPG-NSTCLPCPANKDYGAETAGGATAGGAATLAKOCNIACPDGTA 317
DB 259 TECTNCAPNFYNNAPNFNPG-NSTCLPCPANKDYGAETAGGATAGGAATLAKOCNIACPDGTA 317
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Db 268 -----PGNSKCVACESKKT-NSQSRSGLEANLAAQCQTECPAGT 307
QY 318 IASGAT-NYVILQTECLNCAANFYEDGNFQAGSSRCACAPANKVOGAVATAGGTATLIA 376
Db 308 VTDGVTPTVTSQVCNCKAGFY-QNSNFAGKQCKNCAVSKT-GSASVPGNSATSAT 365
QY 377 QCALECPAGTTLTDTGTTSTYKQAASECVKCAANFYTTKOTDHWAGIDTCTSCNKKLTSGA 436
Db 366 QCONDCPAGTVDDGTSTNFVALASECTKQCNFYASTSGPAAGTDTCTCTECSKKLTSGA 425
QY 437 EANLPESAKKNTQC---DFANFLSLLLSIYLL 468
Db 426 TAKVVAETQKAQCASSSTFAKELSLIFISPYLL 460

RESULT 4
ID Q27208 PRELIMINARY; PRT; 395 AA.
AC Q27208;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Immobilization antigen precursor (Fragment).
OS Ichthyophthirius multifiliis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Ophryoglenina; Ichthyophthirius.
OX NCBI_TaxID=5932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEORGIA;
RX MEDLINE=92335298; PubMed=1631132;
RA Clark T.G., McGraw R.A., Dickerson H.W.;
RT "Developmental expression of surface antigen genes in the parasitic
RT ciliate Ichthyophthirius multifiliis.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6363-6367(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GEORGIA;
RX MEDLINE=93020590; PubMed=1383510;
RA Lin T.L., Dickerson H.W.;
RT "Purification and partial characterization of immobilization antigens
RT from Ichthyophthirius multifiliis.";
RL J. Protozool. 39:457-463(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GEORGIA;
RA Clark T.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; M92907; AAC36158.1; -.
DR PRINTS; PR01574; TUBBYPROTEIN.
KW Signal;
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 395 IMMOBILIZATION ANTIGEN.
SQ SEQUENCE 395 AA; 39567 MW; 68DA2C790E4FD393 CRC64;

Query Match 30.5%; Score 775.5; DB 5; Length 395;
Best Local Similarity 44.2%; Pred. No. 7.9e-49;
Matches 175; Conservative 35; Mismatches 129; Indels 57; Gaps 16;

QY 93 VKCPAGTAAGGATDY-AAITECVNCRINFY-----NENAP--NFNAGASTGTA 139
Db 2 VPCPDGTQAGLTDVGAADLTGCNCRPNFYNGGAQGEANGQNPFAANNAARGICVP 61
QY 140 CPVNRVGGALTAGNATVAQCNVACPTGTALDDGVTYVRSFTCEYKCRNFYNGNN 199
Db 62 CQINRVGSVTNAGDLATLQATCSTQCTGTALDDGVTDFDRSAAQCVKCPNFYNGS 121
QY 200 --GNTP-----FNPG-----KSCQTPCPAIPANVAQATLGNDAITIAQCNVACPDG 244
Db 122 PGEAPGVQVFAAGAAAAGVAATVSCVPCQLNK--NDSPATGAQANLATQCSNQCPGT 179
QY 245 TISAAGVNNVWAQNT-E---CTNCAPNFYNN-----NAPN---FNPNG-----NSTC 283
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Db 180 TVLDDGVT--LVFTSATLVCVKCRPNFYNGSGPQSGAPGVQVFAAGAAAAGVAANTSQC 237
QY 284 LPCPANKDYGAETAGGAATLAKQCNACPDGTGTAIASGAT-NYVILQTECLNCAANFYFD 342
Db 238 VPCQINKN-DSPAATGAQANLATCSTQCTGTATQIDGVTLVFSNSSTQCSOCIANYFFN 296
QY 343 GNNFQASSRCKACAPANKVOGAVATAGGTATLIAQCALECPAGTTLTDTGTTSTYKQAASE 402
Db 297 G-NLEAGKSQCLKCPKSVKTTPAHA-PGNTATQATQCLTCTPAGTVDLDDGTSTNFVASATE 354
QY 403 CVKCAANFYTTKOTDHWAGIDTCTSCNKKLTSGAEA 438
Db 355 CTRCSAGFFASKTGTGTAGTDTCTECTYKLTSGATA 390

RESULT 5
ID Q9GPP0 PRELIMINARY; PRT; 371 AA.
AC Q9GPP0;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE Immobilization antigen LD (Fragment).
GN SERLD.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANF18211;
RX MEDLINE=20549003; PubMed=11095959;
RA Doerder F.P., Gerber C.A.;
RT "Molecular Characterization of the SerL Paralogs of Tetrahymena
RT thermophila.";
RL Biochem. Biophys. Res. Commun. 278:621-626(2000).
DR EMBL; AF312775; AAG38107.1; -.
FT NON_TER 1 1
SQ SEQUENCE 371 AA; 35175 MW; 5817EFPFC2517DEAC CRC64;

Query Match 13.6%; Score 345; DB 5; Length 371;
Best Local Similarity 30.1%; Pred. No. 1.6e-17;
Matches 141; Conservative 41; Mismatches 175; Indels 112; Gaps 33;

QY 8 ILIISLFINQIKSAN-CPVGTETNTAGQVDDLTGPANVCNCKNFYNNAAAFVPGASTC 66
Db 6 LILISLAV--IATVNAAC---TDTNATA-----GAGGTCTF-CNAGYYGTSTDVTAAGA--C 52
QY 67 TPCQKKDAGQNPPTATNLVTCNVKCPAGTAAGATDYAAIITECVNCRINFYNNEN 126
Db 53 QKCPTGTNSVA---ATASGLTVTSCT---CNDTNAGLKADNSG-----COCKANFY--G 98
QY 127 APNENAGAST-CTACPVNRVGGALTAGNAATIVAAQCNVACPTGTALDDGVTYDVRSFTE 185
Db 99 TPNVAVAGATGCTTACP---TGTASPACTAAVTSCAN-----DTNASLKGDNS 143
QY 186 CVKCRNLNFYNGNNGTTPNPNGSKQCTPCPAIPANVAQATLGNDAITIAQCNVACPDGT 245
Db 144 GCCKANFYGTNP-----AVAGGATGCTTACP-----TGSAAGAGSTAVTSCACN-----DT 189
QY 246 ISAAGVNNVWAQNTCTNCAPNFYNNAPNPNPCNSH-CLPCPANKDYGAETAGGAATL 304
Db 190 NSAL-----RADNSACI-CKANFY--GTPNAVAGGATGCTTACPT-----GSAAGASTAVT 237
QY 305 AKQCNACPDGTATASGATNYVILQTECLNCAANFYEDGNFQAGSSRCACAPANKYQGA 364
Db 238 SCACN-----DTNSALKADN-----SACI-CKANFYCTPNVAVAGGATGCTTACPT-----GT 282
QY 365 VATAGGTATLIAQCALECPAGTTLTDTGTTSTYKQAASECVKCAANFYTTKOTDHWAGIDT 424
Db 283 TSTAG--TTVIGSCA--CP-----DTNASLNTATPPVQCNCANFYGTPTTTTGASG--- 328
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Query Match 11.2%; Score 283.5; DB 5; Length 305;
Best Local Similarity 30.1%; Pred. No. 4e-13;
Matches 118; Conservative 34; Mismatches 141; Indels 99; Gaps 29;

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QY 8 ILIISLFINOIKSAN-CPVGTETNTAGVDLCTPANCYNCKNFYNNAAAFVPGASTC 66
DB 6 LILISLAV--IATVNAC---TDTNATA-----GAGGTCTF-CNAG-YIGTSTDVTPSGS-C 52
QY 67 TPCPQKKDAGAPNPATANLVTQCNVKPCPAGTAIAGGATDYAAIITECVNCRINFINEN 126
DB 53 TKCPTGTNSVA---ATASGTLVSSCT--CNDTNASLKGDN-----SGC-QCKANFY--G 98
QY 127 APN-FNAGASTCTACPVNRRVGGALTAGNAATIQAOCNVACPTGTALDDGGVTTDYVRSFTE 185
DB 99 TPNNAVSGGATGCSACP---TGTTSPAGTAATVSCACN-----DTNASLKGDN 143
QY 186 CVKRLNFYNGNGNTPFPNGKSOCTPCPAIKPANVAQATLGNDAITIAOCNVACPDGT 245
DB 144 GCQCKANFYGTPN---AVAGGATGCTACTGSA-----AAGSTAVTSCACNDTN 190
QY 246 ISAAGVNNVAQNTCTNCAPNFYNNAPNPNPNSGT-CLPCPANKDYGAETAGGAATL 304
DB 191 SSLK-----ADNSACY-KRANFY--GTPNAVAGGATGCTACTP-----GTTSTAG--TTV 235
QY 305 AKOCNIACPDGTATASGATNVVILQTECLNCAANFYFDGNNFOAGSSRCKACPANKVQGA 364
DB 236 IGSC--ACPDNTAALNSATPPV-----COCKANFY--GTPTAGSGGCTACTPS-----GQ 281
QY 365 VATAGGATLTAOCALECPAGTVLTDGTTSTY 396
DB 282 TAPA-GSATNVCKAA-----STSTSTY 301
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RESULT 9

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Q24970 ID Q24970 PRELIMINARY; PRT; 594 AA.
AC Q24970;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Variant-specific surface protein.
GN VSPA6-S1.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WBA6;
RX MEDLINE=96010579; PubMed=7581319;
RA Yang Y.M., Adam R.D.;
RT "Analysis of a repeat-containing family of Giardia lamblia variant-
RT specific surface protein genes: diversity through gene duplication and
RT divergence."
RL J. Eukaryot. Microbiol. 42:439-444 (1995).
DR EMBL; U17980; AAA82585.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 594 AA; 59375 MW; 9680818FB75F52AC CRC64;
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Query Match 9.3%; Score 236; DB 5; Length 594;
Best Local Similarity 23.2%; Pred. No. 2.3e-09;
Matches 131; Conservative 47; Mismatches 207; Indels 180; Gaps 32;

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QY 20 SANCPCVGTETNTAGVDLGTTPANCYNCKNF--YNNAAAFVPGASTCTPCPQKKDAGQ 78
DB 40 NGNTPYLKKTNPS---DPTGTCTVSAVDCQGSAGYYTDDS--VSDAKECKK----- 85
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QY 79 PNPP-----ATANLYTQC-----NVKCPAGTAIA-----GGA-----TDYAAIL 112
DB 86 -NAPCTACAGTADKCTKCDANGAAPYLKKTNPDSPTGTCVSAVDCQGSAGIYTTDSVDA 144
QY 113 TCVNCRINFINENAPN-----FNAGASTCTCTACPVNRRVGGALTAGNAATIQAOCNVACP 166
DB 145 KECKKA---EGQKPNTAGTQCFSCSDANCERCQDNDVCARCSTG-APPENGRKCPAATP 199
QY 167 TGTALDDGVTTDYVRSFTE-CVKCRNLNFYNN-----GNNG-----NTPF----- 204
DB 200 GCHSSCDGCTENAMTNQADKCTGCKEGRYLKPESAAAGSGTCLTAECTSDTTHFTKEKA 259
QY 205 NFGKSOCTPCPAIKPA-----NVAQATLGNDAITIAOCNVACPDGTISAAGVNNVAQNT 259
DB 260 GDSKGMCLPCSDATHIAGCKKCALKTLSGEAESTVWCS-ECTDKWLTPSG-----NA 311
QY 260 ECTNCAPNFYNNAPNPNPNSGTCLPCPANKD-----YGAETAGGAATIA 305
DB 312 CLDNCPCAGTYPDNNLCTSCHDTCAECGNADRACSTACYPGYSLLYGS-CTAG---TCV 367
QY 306 KQNTA-----CPDG-----TAI-ASGATNY-VILQTECL 333
DB 368 KECTGAFGANCADGGCTADVGGAKYCAQCKDGYAPIDGICTAVAAAGRTNVCTAADGTCT 427
QY 334 NCAANF-YFDGNF-----QAGSSRCKACPANKVOGAVATAGTATLIAOQAL 380
DB 428 KCAGETLMSGCGYGVAKLPKGSVCTLASNGKICMCAN-----GOAPVQEKCP- 476
QY 381 ECPAG-----TVLTDGTTSTYKQAASECVKCAANFYTTKOTDWWAGIDTC----- 425
DB 477 ECSEGCACKCNDSNACTECLPGYYKGGADKCFCKCTASSGNNGNITGVANCVTCPAPGSG 536
QY 426 -TSCNKKL--TSGAEANLPESAKKN 447
DB 537 SVTCYVKTDTGSGDDNDTGGSVNKS 561
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RESULT 10

```
O97448 ID O97448 PRELIMINARY; PRT; 645 AA.
AC O97448;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cysteine-rich protein.
GN CRP65.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96186899; PubMed=8635746;
RA Chen N., Upcroft J.A., Upcroft P.;
RT "A new cysteine-rich protein-encoding gene family in Giardia
RT duodenalis."
RL Gene 169:33-38 (1996).
DR EMBL; L39804; AAB06228.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00261; FU; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_4.
SQ SEQUENCE 645 AA; 65262 MW; FL9FE98DBB0AA589 CRC64;
```

Query Match 9.1%; Score 232; DB 5; Length 645;
Best Local Similarity 22.9%; Pred. No. 4.9e-09;
Matches 117; Conservative 40; Mismatches 183; Indels 170; Gaps 28;

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QY 19 KSANCPVGTETNTAGVDLGTTPANCYNCKNFYNNAAAFVPGASTCTPC--PQKKDAG 76
DB 176 KASNTDCGEELKRAG-----CATC-----TAVGPNQGTCLTTCNGGQKVLN 216
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QY 77 AONPPATANLVTCQNVKPCAGTATAGGATDYAAIITEVCNCRINFIN-----ENAPNFN 131
Db 217 G-----ISCDCSPSSAAMPD-----ICEC-NEGFLNSGKDCCEKASNTD 257
QY 132 -----AGASTCTACPNVRVGGALTAGNAATIV-----AQCNAVCPGTALDDGVTYDV 180
Db 258 CGEELKRAAGCATCTAVGPN--GOTCLTCNGGQVOLNGISGDCSPSSAAMPDI----- 310
QY 181 RSFTECVKRLNFYNGNG-----NTPFNPGRKSOCTPCPAIKPAN--VAQAT 226
Db 311 -----CECEGFLNSGKDCCEKASNTQNTP-----NCKTCDNPKTDNEVCTECN 356
QY 227 LGNDATITTAQCNAVCPDGTISAGYNNVAQNTNCAPNFYNNAPNFNPGNSTCLPC 286
Db 357 DGDYLTPTNOQVPDCT--TISGYGDN-----DKCKACSPEC-----AECVGPANNQCSSC 406
QY 287 PANK--DYGAETAGGAATLAKOCNACPDGTAIAS-----GATNYVI---LQTE----- 331
Db 407 PAGKLTYYDDSNPNNGGTCGDACKVSA--DGTGCTCGAIGGTAYCCKCTSTQAPLNG 465
QY 332 -----CLNCAANFYF-DG-----NNFQAGSSRCKACPA 358
Db 466 DCAASRATFCTKMGNGVCTOCEDNYFLKDGCGYQTDROPKQVCSNAQGGNGKQCT-- 523
QY 359 NKVOGAVATAGTATLIAQCALECPAGTVLTDGTSTYKQAASECVKCAANFYTTKQTDW 418
Db 524 --ANGLAATDGNCAECHPTCA-----TCSAPSTASSCKTCATGYKENGDDT 568
QY 419 VAGIDTCTSCNKKLTSGAEANLPESAKKNI 448
Db 569 TDG--PCMCKSEKI--SGCKQCVSSSGSVI 595

RESULT 11
Q24977
ID Q24977 PRELIMINARY; PRT: 1274 AA.
AC Q24977
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cysteine rich protein.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen N., Upcroft P., Upcroft J.;
RT "A Giardia duodenalis gene encoding a protein with multiple repeats of
a toxin homologue.";
RL Parasitology 111:0-0(1995).
DR EMBL; L29079; AAA74587.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00181; EGF; 27.
DR SMART; SM00261; FU; 16.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 1274 AA; 135720 MW; 321622872A971A32 CRC64;
```

Query Match 9.0%; Score 228; DB 5; Length 1274;
Best Local Similarity 23.1%; Pred. No. 2e-08;
Matches 119; Conservative 35; Mismatches 183; Indels 178; Gaps 30;

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QY 21 ANCPV-GTETNTAGQVDDLGPANCVNCQKNFYNN-----NAAAFVPGASTCTPC 69
Db 801 APCNVEGCEITVEGNAQ-----QCKTCRPGYINTDTKQCTKDPAPCNVEGCEITCV-- 852
QY 70 PQKDDAGAQP-----NPPATANLVQ-----CNVYK-CPAGTATAGGATDYAAIITEC 115
Db 853 ----EGNAQCKTCRPGYINTDTKQCTKDPAPCNVEGCE--TCVBGNA-----QCC 899
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QY 116 VNCRINFENAPNFNAGASTCTACPNVRVGGALTAGNAATIVAACNVACPTGTALDDGV 175
Db 900 KTCRPGY-----TINTDTKQCTKDP-----EAPCNV-----EGC 928
QY 176 TTDYVRSFTECVKRLNFYNGNG-----NTPFNPGRKSOCTPCPAIKPANVAQA 225
Db 929 ETCVEGNAQCKTCRPGYINTDTKQCTKDPAPCNTP-----NCKTCDNPKTDNEI-C 981
QY 226 TLGNDATITTAQCNAVCPDGTISAGY-----NNVAQNTNCAPNFYNNAPNFNPGN 280
Db 982 TKCNDGDLTPTNOQVPDCT--AISGYGDTDKKCKACNPECAECV-----GPN 1029
QY 281 STCLPCPANK--DYGAETAGGAATLAKOCNIA-----CPD-----GTAISGATN--- 324
Db 1030 NOCTACPVGKMLQYTDINTPVNGTQMDQCSVSTNDGCAECGAQIGGTAYCCKNTQO 1089
QY 325 -----YVILQTECLNCAANFYF-DG-----NNFQAGSSRC 353
Db 1090 APLNGNCAASSRVAFCATITSGACTKNEGYFLKDGCGYQTDROPKQVCSNAQGGNGKC 1149
QY 354 KACPANKVOGAVATAGTATLIAQCALECPAGTVLTDGTSTYKQAASECVKCAANFYTT 413
Db 1150 QTC-----ANGLAASDGNCA-ECHS-----TCAFCST-ADAADCKCTCATGYKE 1192
QY 414 KQTDWVAGIDTCTSCNKKLTSGAEANLPESAKKNI 448
Db 1193 NGDDTTAGL--CKKCKSEKI--SGCKQCVSSSGSVI 1224

RESULT 12
Q9XTK3
ID Q9XTK3 PRELIMINARY; PRT: 667 AA.
AC Q9XTK3
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE VSP417-3/A-II.
GN VSP417-3/A-II.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BRIS/83/HEPU/136;
RX MEDLINE=99053029; PubMed=9836309;
RA Ey P.L., Darby J.M., Mayrhofer G.;
RT "Comparison of ts417-like variant-specific surface protein (VSP)
genes in Giardia intestinalis and identification of a novel locus in
genetic Group II isolates.";
RL Parasitology 117:445-455(1998).
DR EMBL; AF033584; AAD03497.1; -.
DR HSP; P02468; 1TLE.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00261; FU; 3.
SQ SEQUENCE 667 AA; 69123 MW; 77C64CFF59441C0C CRC64;
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Query Match 9.0%; Score 227.5; DB 5; Length 667;
Best Local Similarity 24.3%; Pred. No. 1.1e-08;
Matches 120; Conservative 39; Mismatches 176; Indels 159; Gaps 33;

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QY 18 IKSANCPVCTETNTAGQVDDLGPANCVN---CQKNFYNNAAAFV-----PG 62
Db 171 IKTATC-TGCDSNKIVKTDTSGT--SCITEESACSGFFVSDQQAQSKDYKCIPIRIDPA 227
QY 63 ASCTPCPKQKADAGQPNPPATANLVTCN-----VKCPAGTATAGGAT 106
Db 228 KANCIACSDNK---KPNLEG-----TECNSTCDQHCACFVAEGTCQKSSGILDG--- 275
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QY 107 DYAAIITEC--VNCRINFEYNAPNFENAGASTCTAC-----PVNR-VGALTAGN--A 154
      : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 276 -QNCVKSCKTENCKA-----CTNPKAANEVCTECVTHLTPSQCVQYQCTLGNYYA 328
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 155 AT-----IVACQNV-CPTGALDDGVTTDYVRSFTECVKRLNFYNGNNTPFNPG 207
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 329 CTNADKNACKBCRVANCK--TCVDQG-----QCQTCNNGFYKNGDACSPCHESC 376
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 208 K-----SQCPCPAIPANVAQTALGNATITTAOCNVACPDGTISAAGVNNVAONTE 260
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 377 KTCAGTASDCTKCTGTGKALR-----YGNDDT-RGTCGEGCTTGKSGA----- 419
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 261 CTNCAPFEYNNAPNFENPGNSTCLPCPANKDYG-----AEATAGAAATLAKOCNIA---- 311
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 420 CKTCGLTI-----DGASYCSECATTEYPQNGICTSTTARTAT-CKNSNVANGIC 469
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 312 -CPDGTAIAGS-----ATNY-----VILQT-----ECLNCAANFYDG-NNFOAGSSRCKAC 356
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 470 SLCTNGFLRMNGGCYETTKFPKGSVCTTTPDADTCTSVTSGYYIDGSSNLVVCSDGCAEC 529
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 357 PANKVOGAVATAGGTATLI--AOCALCPAGTDLTDTGTTSTYKQAASECVKCAANFYTK 414
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 530 TTS-----SACTCKDGTYKIGNSQCTKC-----DSSCETCTGAATCKACATGYTKT- 578
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 415 QTDWVAGIDTCTSC 428
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 579 ----ALGESTCTSC 588
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
Q9U019 PRELIMINARY; PRT; 719 AA.
AC Q9U019;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Variant-specific surface protein.
GN VSP417-7.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRIS-136;
RA Ey P.L., Darby J.M.;
RT "A new locus (vsp417-7) belonging to the subfamily of tsa417-like
variant-specific surface protein (vsp) genes in Giardia
intestinalis."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067148; AAF21772.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 2.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 4.
SQ SEQUENCE 719 AA; 73874 MW; E409450249E3F716 CRC64;

Query Match 8.9%; Score 226; DB 5; Length 719;
Best Local Similarity 23.3%; Pred. No. 1.5e-08;
Matches 109; Conservative 40; Mismatches 178; Indels 140; Gaps 25;

QY 44 CVNCKNFY-----NNAAAFVPGASTCTPCP-----QKKDAGAQPNPPATANLVTCNV 93
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 264 CDDTKGFKYKVDSTNGKVCSCDAGAGLAVGADGAWKGVDCAKCTKPADINTPTKCD- 322
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 94 KCPAGTAIAGGATDYAALITECV-----NCRINFEYNAPNFENAGASTCTACPVN----- 143
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 323 ECKPGYEI---STDK-----TKTSTAPPCPI-----ENCKVCSBKCRACECSNNYLTP 371
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 144 -----RVGGALTAGNA-----ATIVAOCNVACPTGT--ALDDGVTTDYVRSFTE 185
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db 372 TRMCIDCKKIGNYYTTNANKKLICKECAVANCKECENTGCTCKTCDG-----FYKSSEE 427
QY 186 CVKRLNFYNGNNGNTPFNPGSKSQCTPCPAIPANVAQTALGNATITTAOCNVACPDGT 245
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 428 CKACDSN--CKTCNGGT-----SADCTKC-----LSGAVLKVYNGDDT-RGTCGAGCATGT 474
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 246 ISAAGVNNVAQNTCTNCAPNFENNNAPNFENPGNSTCLPCPANKDY-----GA 294
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 475 GAGA-----CKTCG-----LIIDGTSYCSSECAVETEPGGVCSSTTVRA 514
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 295 EATAGGAATLAKOCNTACPDG-----TAIASGATNYVILQTECL 333
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 515 AATCKAGSVAKGNCN-SCINGFLRMNGGCYETTKFPKGSVCBEAASAGDT-----CQ 565
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 334 NCAANFYFDGNTFOAGSSRCKACPAKV-----QGAVATAGGTATLIAOCALCPAGTVL 398
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 566 KEAPGYHLNNDLVTCSPGCKTCTSNVTCTACMEGYVTKSDSCAKAAGCA-TCTGSTTA 624
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 389 TDGTTSTYKQAASECVKCAANFYTTKQTD--WVAGIDTCTSCNKKLTS 434
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 625 CDTCSTGYESGTCVSC-----TESNCKTIITGVANCASCAPPLNN 666
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
Q9U021 PRELIMINARY; PRT; 719 AA.
AC Q9U021;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Variant-specific surface protein.
GN VSP417-7.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD-1;
RA Ey P.L., Darby J.M.;
RT "Comparative analysis of the VSP417 subfamily of variant-specific
proteins in Giardia intestinalis."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF189719; AAF04387.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 2.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 4.
SQ SEQUENCE 719 AA; 73888 MW; 83BE706BACE7F977 CRC64;

Query Match 8.7%; Score 221.5; DB 5; Length 719;
Best Local Similarity 23.1%; Pred. No. 3.2e-08;
Matches 113; Conservative 40; Mismatches 176; Indels 161; Gaps 28;

QY 27 TETNTAGQVDDL-----GTPAN-CVNCKNFYNNAAAFV-----PGASTCTPCP 70
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 256 TECVAANECDTQKGFYKVDSTNGKVCSCA-----DGAGLAVGTDGAWKGVDCAKCI 310
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 71 OKKDAQAQNPPATANLVTCNVKCPAGTAIAGGATDYAALITECV-----NCRINFEYNE 125
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 311 K-----PADINTPTKCD-ECKPGYEI---STDK-----TKTSTSTAPPCPI-----E 348
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 126 NAPNFENAGASTCTACPVN-----RVGGALTAGNA-----ATIVAOCNV 164
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 349 NCKVCSBKCRACECSNNYLTPTRMCIDCKKIGNYYTTSNANKKLICKECAVANCKEC 408
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 165 CPTGT--ALDDGVTTDYVRSFTECVKRLNFYNGNNGNTPFNPGSKSQCTPCPAIPANV 222
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 409 ENTGCTCKTCDG---FYKSSECKACDSN--CKTCNGGT-----SADCTKC-----LSG 452
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 223 AQTALGNATITTAOCNVACPDGTISAAGVNNVAQNTCTNCAPNFENNNAPNFENPGNST 282
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db 453 AVLYGNDGT-KGTCGAGCATGTGAGA-----CKTCG-----LIIDGTSY 491
Qy 283 CLPCPANKDY-----GAEATAGGAATLAKQCNIACPDG----- 315
Db 492 CSECAVETEPQGGVCSSTTVRAAATCKAGSVAGMCN-SCTNGLFMRMNGGCVETTKFPG 550
Qy 316 -----TAIASGATNVILQTECLNCAANFYFDGNNFQAGSSRCACAPANKV-----QGAV 365
Db 551 KSVCEEAASAGDT-----CQEAFCYHLNNDLVTCSPGCKTCTSNIVCTACMEGYV 602
Qy 366 ATAGGTATLIAQCALECPAGTTLTDTSTYKQAASECVKCAANFYTTKTD-WVAGIDT 424
Db 603 KTDSCAKAAGCA-TCTGSGTTACDTCSTGYKSGTTCVSC-----TESNSDKTITGVAN 656
Qy 425 CTCNKKLTS 434
Db 657 CAXCAPPLNN 666

RESULT 15
Q9NGL3 PRELIMINARY; PRT; 1274 AA.
ID Q9NGL3 AC Q9NGL3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE variant-specific surface protein VSP136b.
GN VSP136b.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AD-1;
RA Mansouri M., Ey P.L.;
RT "Analysis of a vsp136 homolog in Giardia intestinalis.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249878; AAF69839.1; -.
DR InterPro; IPR000345; Cytc_heme_bind.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR005127; Giardia_VSP.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00181; EGF; 23.
DR SMART; SM00261; FU; 14.
DR PROSITE; PS00190; CVTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 1274 AA; 135671 MW; 68644A814BD6AE65 CRC64;

Query Match 8.6%; Score 219; DB 5; Length 1274;
Best Local Similarity 22.9%; Pred. No. 8.9e-08;
Matches 118; Conservative 35; Mismatches 184; Indels 178; Gaps 30;

Qy 21 ANCPV-GTETNTAGQVDDLTGPANCVNCKNFYNN-----NAAAFVPGASTCTPC 69
Db 801 APCNVGECCTCVGNAQ-----QCKTCRPGYTINTDTKQCKDPEAPCNVEGCTCV-- 852
Qy 70 POKKDAGAPQ-----NPPATANLVQ-----CNVK-CPAGTAIAGGATDYAAIITEC 115
Db 853 -----EGNAQCKTCRPGYTINTDTKQCKDPEAPCNVEGCE--TCVVGNA-----QQC 899
Qy 116 VNCINFYNENAPNAGASTCTACPNVNRVGALTAGNAATIVAOQNVACPTGTALDDGV 175
Db 900 KTCRPGY-----TINTDTKQCKD-----EAPCNV-----EGC 928
Qy 176 TTDYVRSFTECKVCFNLNFYNNNG-----NTPFNGKSOCTPCPAIKPANVAQA 225
Db 929 EFCVEGNAQCKTCRPGYTINTDTKQCKDPEAPCNTP-----NCKTDNPKTDNEL-C 981
Qy 226 TLGNDATITAOQNVACPDGTISAAGV-----NNWVAQNETCTNCAPNFNNAPNFPNGN 280
Db 982 TKCNDGDYLTPTNQCVPDCT-AISGYGDTDKKACNPECAECV-----GPN 1029
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Qy 281 STCLPCPANK--DYGAETAGGAATLAKQCNIA-----CPD-----GTATASGATN--- 324
Db 1030 NQCTACPVGKMLQYTDNTNTPVNGGTCMDQC SVSSTNDGCAEGGAIGGTAYCCKNTQQ 1089
Qy 325 -----YVILQTECLNCAANFYF-DG-----NNFOAGSSRC 353
Db 1090 APLNGNCAASSRVAFCAITTSAGCTKCNBEGYFLKDGCGYQTDROPKGQVCSNAQGGNGKC 1149
Qy 354 KACPANKVOGAVATAGGTATLIAQCALECPAGTTLTDTSTYKQAASECVKCAANFYTT 413
Db 1150 QTC-----ANGLAASDGNCA-ECHS-----TCATCST-ADAADCKCTCATGYNKE 1192
Qy 414 KQTDWVAGIDTCTSNKKLTSGAEANLPESAKNNI 448
Db 1193 NGDDTTTAGL--CKKCKSEKI-SGCKQCVSSSGSVI 1224

Search completed: February 11, 2003, 19:47:55
Job time : 33.3429 secs
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